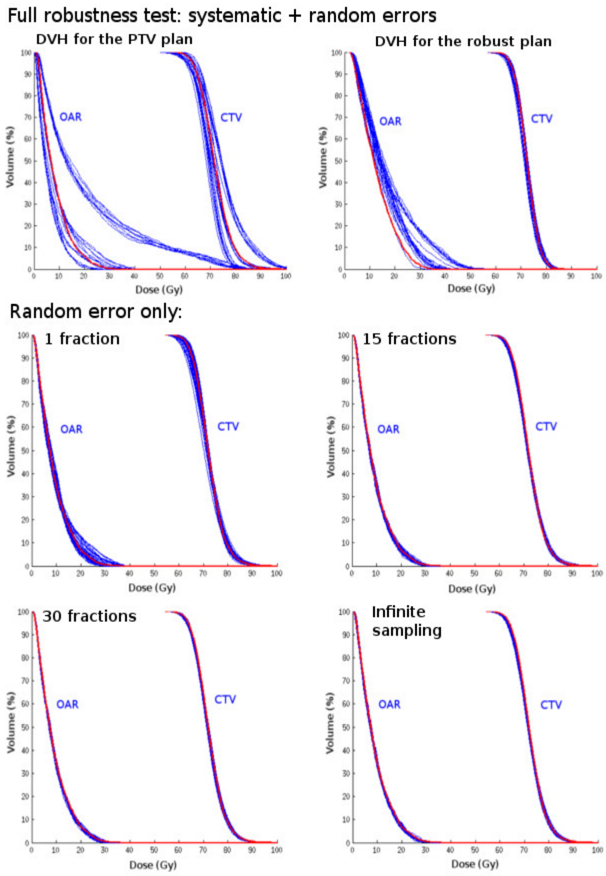


**Conclusions:** Fast and accurate MC tools allow range uncertainties to be reduced and random errors to be integrated efficiently into robustness evaluation. In proton therapy, robust optimization is preferred to traditional PTV margins, which do not suffice to ensure homogeneous coverage of the CTV in case of uncertainties.

**PO-0888 Evaluation of 6 proton dose calculation algorithms using a critical experimental phantom**

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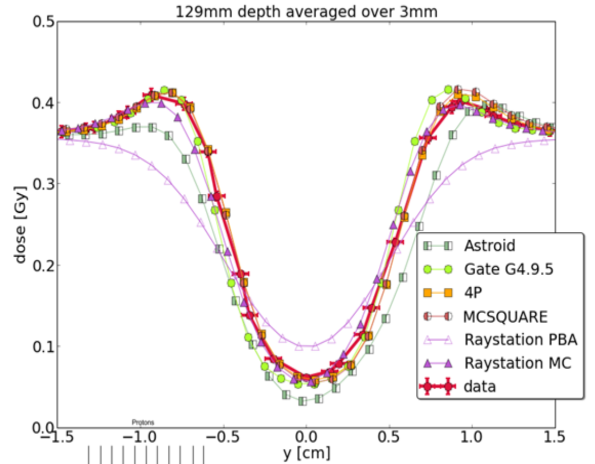
**Purpose/Objective:** Pencil Beam Scanning (PBS) delivery enables intensity modulation and has showed a promising potential to improve radiotherapy treatments. However, the dose distributions are very sensitive to range uncertainties. In highly heterogeneous anatomies, range uncertainties can be significantly reduced using Monte Carlo (MC) simulations for dose calculation. Nevertheless, MC is usually too time consuming for clinical practice and it is common to use dose engines based on faster but less accurate analytical models. Lateral inhomogeneities may have a strong influence on the dose distributions depending on how accurate the modeling of proton multiple scattering is. Here, we devised an experimental design in order to maximize this effect and study the behavior of six different dose calculation codes.

**Materials and Methods:** The inhomogeneous phantom is composed of a water phantom with a 1x10x10cm³ sliver of bone equivalent material (Gammex SB3) inserted at the center of the phantom. PMMA plates are placed downstream the water-bone box. The beam direction is parallel to the bone sliver. The nominal proton range is 18 g.cm$^{-2}$ and the composite field size is 10x10 cm² (fig 1 left). Data are acquired at different depths with a 2D ion chamber array (MatriXX, IBA) for a universal nozzle (MGH, Boston) in PBS mode. Absolute dose measurement is compared to Astroid (by .decimal). Taking advantage of the homogeneous dose region around the bone slab, relative comparisons with five other simulations are performed using: Gate (Geant4 9.5), 4P (Penelope for protons), MCSQUARE, the pencil beam algorithm (PBA) and the future MC (non-clinical) of the RayStation (Raysearch Lab.). Beam models used are close to the MGH beam model.

**Results:** Simulations are compared to data at 129 mm depth and averaged over 3mm in the y-direction to take into account the spatial resolution of an ion chamber (MattriX). Symmetric 1D Gamma evaluations (Yepes, PMB 2014) are performed to measure differences. MC codes have higher local g-index passing rates than the analytical computation algorithms. 4P shows the best agreement with data regarding gamma indexes. Astroid and Raystation-PBA have g-index passing rates lower than 50%. MCSQUARE and Raystation-MC are within 82.73% and 77.81% for the 5%/3mm criteria. Those codes offer computation times competitive in clinical routine.



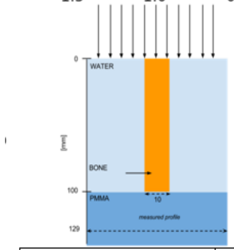




**Figure 1.** Schematic view of the experimental set-up and dose profiles at 129mm depth averaged over 4mm for experimental data (red circles), Astroid (left filled green squares), Gate G4.9.5 (green circles), 4P (orange squares), MCSQUARE (left filled red circles), Raystation PBA (purple triangles) and Raystation MC (filled triangles).

| Table 1. γ-index passing rates [%] | 5%/3mm | 5%/1mm | 3%/3mm | 3%/1mm | 2%/2mm |
|---|---|---|---|---|---|
| Astroid (PBA) | 50.46 | 50.46 | 40.37 | 40.37 | 37.46 |
| Gate | 69.69 | 65.31 | 68.13 | 60.94 | 62.81 |
| 4P | 84.29 | 79.85 | 82.98 | 76.97 | 68.83 |
| MCSQUARE | 82.73 | 81.17 | 71.22 | 65.46 | 64.14 |
| Raystation PBA | 37.19 | 34.69 | 30.31 | 25 | 17.81 |
| Raystation MC | 77.81 | 70.94 | 73.75 | 67.19 | 65.31 |

**Conclusions:** An experimental set-up for dose determination in heterogeneous media in proton beam therapy was developed. Various dose engines using different techniques and computer technologies were compared to data. Overall, MC simulations show better agreement with experimental data than pencil beam algorithms, including the superfast MCSQUARE and Raysearch-MC, which is promising for future clinical use. The data obtained in the phantom experiment will be used as a basis to interpret disagreements between dose distributions calculated by MC and analytical algorithms in clinical cases.

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**PO-0889**

**A multi-institutional study for the evaluation of DIR algorithms for structure delineation in virtual phantoms**

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**Purpose/Objective:** This study investigates the accuracy of various algorithms for deformable image registration (DIR), to propagate regions of interest (ROIs) in virtual phantoms using different commercial systems. This work is a preliminary step to provide a consistent quality assurance check among different institutions on the use of DIR before its clinical implementation for ROIs and dose propagation in adaptive radiotherapy.

**Materials and Methods:** Ten Italian institutions with 4 available commercial solutions provided data to assess the agreement of DIR-propagated ROIs with automatically drown ROIs considered as ground-truth for the comparison. The DIR algorithms were tested on a specific virtual phantom made of three cylinders of different gray density inside a uniform cube phantom (CT1, Fig 1a) with two data sets obtained by specific Deformation Vector Field (DVF) applied to the reference data set (CT2 and CT3). The different software used in this study are based on various algorithms: a multi-resolution modified basis Spline (B-Spline), a radial basis function, an intensity-based free-form, an Hybrid intensity and structure based and a Biomechanical model based. The DIR-mapped ROIs were then compared with the reference ROIs using the Dice Similarity Coefficent (DSC) and the Mean of the Hausdorff Distance (MHD).

**Results:** Figure 1a shows examples of the DIR-propagated ROIs while figure 1b shows the DSC for the three considered ROIs. Mean values for DSC were 0.93±0.08, 0.94±0.04 and 0.92±0.12 respectively for the three considered ROIs (Cylinder 1, Cylinder 2 and Cylinder 3) on CT2; 0.93±0.08, 0.94±0.04 and 0.94±0.11 were the average values on CT3. Regarding MHD values we obtain 0.14±0.23, 0.19±0.31 and 0.22±0.47 for CT2 while 0.09±0.15, 0.08±0.06 and 0.17±0.39 are the values obtained for CT3. Minimum and maximum values for DSC and MHD resulted respectively 0.65 and 1.23mm

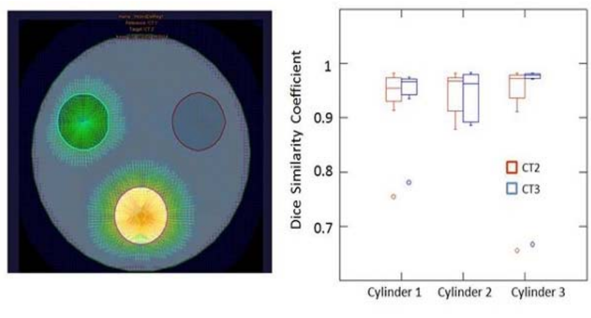


Figure 1. a) b)

**Conclusions:** Although the different algorithms used in this study are significantly dissimilar in their approach to